

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 12, 2003, 15:28:05 ; Search time 30 Seconds  
(without alignments)  
130,497 Million cell updates/sec

Title: US-09-869-540A-2

Perfect score: 113  
Sequence: 1 DFDMLRCMLGRVYRRCMOV 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	db	ID	Description
1	113	100.0	77	6	Q9TTS8	Q9TTS8 sus scrofa
2	113	100.0	165	4	Q8WVG0	Q8WVG0 homo sapien
3	113	100.0	165	11	Q9D220	Q9D220 mus musculus
4	99	87.6	150	13	Q919L6	Q919L6 paratichthy
5	92	83.2	86	4	Q9B0D1	Q9B0D1 homo sapien
6	88	78.8	86	4	Q9B0D1	Q9B0D1 homo sapien
7	48	42.5	250	16	P71972	P71972 mycobacteri
8	46	40.7	166	10	Q9ASL5	Q9ASL5 oryza sativ
9	45.5	40.3	603	10	Q80613	Q80613 arabidopsis
10	45.5	39.8	85	11	Q88259	Q88259 mus musculus
11	45	39.8	342	16	Q8XVC6	Q8XVC6 rlistonias
12	44.5	39.4	386	12	Q9J892	Q9J892 spodioplera
13	44.5	39.4	186	16	Q8XZX6	Q8XZX6 escherichia
14	44	38.9	103	6	Q95LLO	Q95LLO macaca fasc
15	44	38.9	153	2	Q85392	Q85392 coxiella bu
16	44	38.9	154	11	Q9D3R4	Q9D3R4 mus musculus

17	44	38.9	1511	5 Q9VB21	Q9VB21 drosophila
18	43.5	38.5	397	5 Q76862	Q76862 drosophila
19	43.5	38.5	414	5 Q9W4M4	Q9W4M4 drosophila
20	43.5	38.5	524	11 Q8R1L0	Q8R1L0 mus musculu
21	43.5	38.5	640	11 Q8VBW1	Q8VBW1 mus musculu
22	43.5	38.5	732	4 Q13032	Q13032 homo sapien
23	43.5	38.1	253	4 Q9H7E8	Q9H7E8 homo sapien
24	43	38.1	441	10 Q8XP4	Q8XP4 arabidopsi
25	43	38.1	456	10 Q9FKS9	Q9FKS9 arabidopsi
26	42.5	37.6	65	6 Q932E	Q932E sus scrofa
27	42	37.2	86	5 Q8SXZ8	Q8SXZ8 drosophila
28	42	37.2	233	4 Q14862	Q14862 homo sapien
29	42	37.2	270	17 Q97YW2	Q97YW2 sulfolobus
30	42	37.2	311	5 Q9GS12	Q9GS12 ceenorhabdi
31	42	37.2	331	12 Q91TU4	Q91TU4 tupala herp
32	42	37.2	352	11 Q920M2	Q920M2 rattus norv
33	42	37.2	466	16 Q99TH7	Q99TH7 ataphylococ
34	42	37.2	555	12 Q91HR4	Q91HR4 pseudorabie
35	42	37.2	558	12 Q91HR5	Q91HR5 pseudorabie
36	42	37.2	577	12 Q93FE7	Q93FE7 pseudorabie
37	42	37.2	578	12 Q9PTC0	Q9PTC0 pseudorabie
38	42	37.2	708	10 Q9FZ61	Q9FZ61 arabidopsi
39	42	37.2	1489	16 Q8U9P5	Q8U9P5 agrobacteri
40	42	37.2	1497	5 Q95YH6	Q95YH6 drosophila
41	42	37.2	1571	5 Q95YH7	Q95YH7 drosophila
42	42	37.2	1612	5 Q9VE37	Q9VE37 drosophila
43	42	37.2	2749	10 Q8SA93	Q8SA93 zea mays (m
44	41.5	36.7	349	2 Q93KZ0	Q93KZ0 burkholderi
45	41.5	36.7	486	10 Q9FHB6	Q9FHB6 arabidopsi

## ALIGNMENTS

### RESULT 1

ID	Q9TTS8	PRELIMINARY:	PRT:	77 AA.
AC	Q9TTS8			
DT	01-MAY-2000 (TREMURel. 13, Created)			
DT	01-MAY-2000 (TREMURel. 13, Last sequence update)			
DT	01-JUN-2002 (TREMURel. 21, Last annotation update)			
DE	Melanin-concentrating hormone (Fragment).			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=HYPOPHALMUS;			
RA	Wattieri R.L., Dyer C.J.;			
RT	*Partial cDNA sequence of porcine melanin-concentrating hormone			
RT	(MCH).*			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF203034; AAF09587.1; -			
DR	PRINTS; PR01641; PROMCHFAMILY.			
FT	NON_TER	1		
FT	CHAIN	59	>77	
FT	NON_TER	77		
FT	SEQUENCE	77 AA;	8861 MW;	CB640E22E4CF321 CRC64;
SO				MELANIN-CONCENTRATING HORMONE.
QY				
DB	1 DFDMLRCMLGRVYRRCMOV 19			
	59 DFDMLRCMLGRVYRRCMOV 77			
Query Match		100.0%;	Score 113;	DB 6;
Best Local Similarity		100.0%;	Pred. No. 9.6e-12;	Length 77;
Matches	19;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
RESULT 2				
Q8WVG0		PRELIMINARY;	PRT;	165 AA.
ID	Q8WVG0			
AC	Q8WVG0;			

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DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 18.7 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC018048; AAL18048.1;
DR PRINTS: PR01641; PROMCHFAMILY.
KM Hypothetical protein.
SQ SEQUENCE 165 AA; 18679 MW; 23398938BEEC499 CRC64;

Query Match 100.0%; Score 113; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 147 DFDMLRCMIGRYRRCMOV 165

RESULT 3
09BD20 PRELIMINARY; PRT; 165 AA.
AC 09BD20;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE A230109K33R1K.
GN A230109K33R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HYPOPHALANUS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Iwasa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons F., Marchionni L., Mashima J., Marzarelli J., Monbarts P.,
RA Norone P., Ning B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata S., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohauti S.,
RA Hayashizaki Y.;
RT *Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
DR EMBL: AK070723; BAB32189.1;
DR MGD: MGI:1925014; A230109K33R1K.
DR PRINTS: PR01641; PROMCHFAMILY.
SQ SEQUENCE 165 AA; 18516 MW; 1872B6B1D4BEEAC2 CRC64;

Query Match 100.0%; Score 113; DB 11; Length 165;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 DFDMLRCMIGRYRRCMOV 19
DB 147 DFDMLRCMIGRYRRCMOV 165

RESULT 4
0919L6 PRELIMINARY; PRT; 150 AA.
AC 0919L6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Melanin-concentrating hormone-like protein.
OS Paratichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paratichthyidae; Paratichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Jeon J., Lee J., Song Y.;
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF236090; AAF67166.1;
DR PRINTS: PR01641; PROMCHFAMILY.
SQ SEQUENCE 150 AA; 16913 MW; 117A280F46ED4499 CRC64;

Query Match 87.6%; Score 99; DB 13; Length 150;
Best Local Similarity 83.3%; Pred. No. 4.4e-09;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFDMLRCMIGRYRRCMOV 18
DB 128 DFDMLRCMIGRYRRCMOV 145

RESULT 5
09BOD1 PRELIMINARY; PRT; 86 AA.
AC 09BOD1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Pro-melanin-concentrating hormone-like 2 protein.
GN PMCHL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=21108351; PubMed=11181993;
RA Courseaux A., Nahon J.L.;
RT *Birth of two chimeric genes in the Homnidae lineage.*;
RL Science 291:1293-1297(2001).
DR EMBL: AY008413; AAK31297.1;
DR EMBL: AY008430; AAK31290.1;
DR EMBL: AY008412; AAK31296.1;
DR PRINTS: PR01641; PROMCHFAMILY.
SQ SEQUENCE 86 AA; 9856 MW; 1C8D69B786B47471 CRC64;

Query Match 83.2%; Score 94; DB 4; Length 86;
Best Local Similarity 84.2%; Pred. No. 1.8e-08;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DFDMLRCMIGRYRRCMOV 19
DB 68 DFDMLRCMIGRYRRCMOV 86

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<b>RESULT 6</b>					
ID	09B010	PRELIMINARY;	PRT:	86 AA.	
AC	Q9B010				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
D7	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
D7	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Pro-melanin-concentrating hormone-like 1 protein. PMCHL1.				
GN	Homo sapiens (Human).				
OS	Homo sapiens Chordata; Craniata; Vertebrata; Euteleostomi; Olfactores; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NBLT_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=TESTIS;				
RX	MEDLINE=21108351; PubMed=11181993;				
RA	Coureaux A., Nahon J.L.; "Birth of two chimeric genes in the Homnidae lineage.";				
RL	Science 291:1293-1297(2001).				
DR	EMBL: AY008411; AAAK1295.1; -				
DR	EMBL: AY028318; AAAK1289.1; -				
DR	PRINTS: PR01641; PROMCHFAILY.				
SQ	SEQUENCE 86 AA; 9715 KM; BCSECA70BDABF7F3 CRC64;				
Query Match					
Best Local Similarity	78.8%; Score 89; DB 4; Length 86;				
Matches	15; Conservative 1; Mismatches 3; Indels 0; Gaps				
OY	1 DFDMLRCMGLHRYRPPCQV 19            :				
Db	68 DFDLSCMLGRHYGSCMQV 86				
<b>RESULT 7</b>					
ID	P71972	PRELIMINARY;	PRT:	250 AA.	
AC	P71972;				
DT	01-JAN-1998 (TREMBLrel. 05, Created)				
D7	01-JAN-1998 (TREMBLrel. 05, Last sequence update)				
D7	01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE	Hypothetical protein RV2675C.				
GN	RV2675C OR MTGY441.44C OR MTJ7749.				
OS	Mycobacterium tuberculosis.				
OC	Bacteria; Firmicutes; Corynebacteriaceae; Mycobacteriales; Mycobacterium.				
OX	NBLT_TaxID=1773;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-H37RV;				
RX	MEDLINE=98295987; PubMed=9634230;				
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigemeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies K., Devlin K., Felwell T., Gentles S., Hamlin N., Holtroyd S., Hornsbay T., Jagels K., Krug A., McLean J., Moule S., Murphy L., Oliver S., Osborne K., Quill M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;				
RL	"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."				
RT	Nature 393:537-544(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CDC 1551 / OSHKOSH;				
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.F., Deboy R., Dodson R., Gwin M.L., Haft D., Hickey E., Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bisbal M.;				
RA	"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."				
RT	Submitted (APR-2001) to the EMBL/Genbank/DBD databases.				

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-1- SIMILARITY: STRONG, IN C-TERMINAL REGION TO M.LEPRAE U1764Z.
DR EMBL: Z80225; CAB02328.1; -.
DR EMBL: AE007105; AAK47064.1; -.
DR TIGR: MT2749; -.
DR TruSculist; rv2675c; -.
DR Interpro: IPR00051; SAM_bind.
KW Hypothetical protein, Complete proteome.
SQ SEQUENCE 250 AA; 27545 MW; 2EC9718C7550F32C CRC64;

Query Match 42.5%; Score 48; DB 16; Length 250;
Best Local Similarity 34.5%; Pred. No. 3,4;
Matches 10; Conservative 4; Mismatches 3; Indels 12; Gaps

OY 3 DMLRCML-----GRVYRPMCV 19
DB 216 DQVRCVLERFRAIRPMVYGRVAPMEV 244
|:|:|
|:|:|

RESULT 8
O9ASL5 PRELIMINARY; PRT; 166 AA.
O9ASL5;
AC 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE P0554D10.32 protein (P0489E06.10 protein).
DE P0534D10.32 OR P0489E06.10.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-CV, NIPPONBARE;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RA "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0489E06."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002869; BAB39248.1; -.
DR EMBL: AP003143; BAB55782.1; -.
SQ SEQUENCE 166 AA; 18181 MW; 58B03BA8302793CC CRC64;

Query Match 40.7%; Score 46; DB 10; Length 166;
Best Local Similarity 50.0%; Pred. No. 5;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps

OY 1 DFDMLRCMLGRVYRPMCV 18
DB 8 DGDMLATRRGSLHRRPMQ 25
|:|:|
|:|:|

RESULT 9
O80613 PRELIMINARY; PRT; 603 AA.
O80613;
AC 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ATG02980 protein.
GN ATG02980.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

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SEQ SEQUENCE 386 AA; 45719 MW; 6CD83CFAC82CC5AB CRC64;

Query Match 39.8%; Score 45; DB 12; Length 386;

Best Local Similarity 46.7%; Pred. No. 17;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 3 DMLRMLGRVRYPCW 17

DB 254 DQECILEFNYFCW 268

RESULT 13

08X2X6 PRELIMINARY; PRT: 186 AA.

AC 08X2X6

DT 01-MAR-2002 (TREMBLER, 20, Created)

DT 01-MAR-2002 (TREMBLER, 20, Last sequence update)

DE 01-MAR-2002 (TREMBLER, 20, Last annotation update)

OS EC84988.

OC Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI\_TaxID=83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-O157:H7 / RMD 0509952;

RC MEDLINE-21156231; PubMed-11258796;

RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsuka E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,

RA Kihara S., Shiba T., Hattori M., Shinagawa H.;

RT \*Complete genome sequence of enterohemorrhagic Escherichia coli

RT O157:H7 and genomic comparison with a laboratory strain K-12.\*;

RL DNA Res. 8:11-22(2001).

DR EMBL; AF002567; BAB38411.1;

DR Hypothetical protein.

SO SEQUENCE 186 AA; 21454 MW; C5DEDE1B6B8CA9989 CRC64;

Query Match 39.4%; Score 44.5; DB 16; Length 186;

Best Local Similarity 57.1%; Pred. No. 10;

Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 5 LRCMLGRVRYPCW 18

DB 159 LECTINR-TKPMO 171

RESULT 14

095LLO PRELIMINARY; PRT: 103 AA.

AC 095LLO

DT 01-DEC-2001 (TREMBLER, 19, Created)

DT 01-DEC-2001 (TREMBLER, 19, Last sequence update)

DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)

DE Hypothetical 11.3 kDa protein.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

OX NCBI\_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-TESTIS.

RA Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,

RA Terao K., Sugano S.;

RT \*Isolation of novel full-length cDNA clones from macaque testis cDNA

RT libraries.\*;

RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB072778; BAB69747.1;

KW Hypothetical protein.

SO SEQUENCE 103 AA; 11326 MW; D8547BDDA414195 CRC64;

Query Match 38.9%; Score 44; DB 6; Length 103;

Best Local Similarity 31.6%; Pred. No. 6.8; 7; Indels 0; Gaps 0;

Matches 6; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 DFDMLRMLGRVRYPCW 19

DB 46 EYSLDSCDLGLSNPCWRL 64

RESULT 15

085392 PRELIMINARY; PRT: 153 AA.

AC 085392

DT 01-NOV-1998 (TREMBLER, 08, Created)

DT 01-NOV-1998 (TREMBLER, 08, Last sequence update)

DE 01-DEC-2001 (TREMBLER, 19, Last annotation update)

OS Coxiella burnetii.

OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;

OC Coxiella group; Coxiella.

OX NCBI\_TaxID=777;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-NINE MILE PHASE I;

RC MEDLINE-98348442; PubMed-9683477;

RA Williams R., Jaeger C., Baljer G.;

RA \*Physical and genetic map of the obligate intracellular bacterium

RT Coxiella burnetii.\*;

RL J. Bacteriol. 180:3816-3822(1998).

DR EMBL; AF064950; AAD09933.1;

DR InterPro; IPR002606; FAD\_Synth.

DR Pfam; PF01687; FAD\_Synth. 1.

DR Prodom; PD003662; FAD\_Synth. 1.

KW Kinase.

SO SEQUENCE 153 AA; 16978 MW; B58381B46B34789 CRC64;

Query Match 38.9%; Score 44; DB 2; Length 153;

Best Local Similarity 42.1%; Pred. No. 10;

Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 DFDMLRMLGRVRYPCW 19

DB 65 DMAYMALGRPYRLGRV 83

Search completed: June 12, 2003, 15:31:26

Job time : 34 secs